

Query Match	Best Local Similarity	Score	DB	Length
Matches 3733; Conservative	91.8%;	3638.6;	9;	3751;
	98.9%;	Pred. No. 0;		
	0;	Mismatches 14;	Indels 26;	Gaps 6
QY	181	CCCGGGTCGGACGCGCTGGGTCTGCCGGGAAGCGGATGAGAGTGTGTGAAGGTGGCTAT	240	
Db	2	CCGGGTCGGACCGCTGGGTGTGCCGGGAAGGAGTGAAGTGTGTGAAGGTGGCTAT	61	
QY	241	TCACTGAGCGATGGGGTTGACTTTGAAGGAATGCCAAGAGATGCTGCCACCCACCCCTTA	300	
Db	62	TCACTGAGCGAGGGGGTTGACTTTGAAGGAATGCCAAGATGCTGCCACCCACCCCTTA	121	
QY	301	GGCGCGAGGGATCAGAGACTATGGGACCAAGGCCGTATCTTATCTGCTGCTCTT	360	
Db	122	GGCGCGAGGGATCAGAGACTATGGGACCAAGGCCGTATCTTATCTGCTGCTCTT	181	
QY	361	TGGTGCAAGTGGAGATCTGACATGAAGGGACATTTTGAATCCTGCCAATGGCCGTATG	420	

Db 182 TGTGGCAAGTGGAGATGCTGACATGAAGGACATTTGATCCCTGCCAAGTCCGCTATG 241
 QY 421 CCCCTGGGCAATGAGAGACCCGAGACCATCCCAAGATGATCTCTGTTCCAGTCTCGGT 480
 Db 242 CCCCTGGGCAATGAGAGACCCGAGACCATCCCAAGATGATCTCTGTTCCAGTCTCGGT 301
 QY 481 CAGATTCACATGCGCCGCGCACAGAGTGGAGACAGTGGAGGAGTGGGGCTGGT 540
 Db 302 CAGATTCACATGCGCCGCGCACAGAGTGGAGACAGTGGAGGAGTGGGGCTGGT 361
 QY 541 GCCCGGAGGAGTGGTGGTTCCTCCAGAGAGAGTACTTGCAGTGGATCTACAAAGAC 600
 Db 362 GCCCGGAGGAGTGGTGGTTCCTCCAGAGAGAGTACTTGCAGTGGATCTACAAAGAC 421
 QY 601 TCCACCTGGTGGTCTCTGTTGGGACACCCAGAGAGAGTGGCGGGGGCTGGGCAAGAGT 660
 Db 422 TGCACCTGGTGGTCTCTGTTGGGACACCCAGAGAGAGTGGCGGGGGCTGGGCAAGAGT 481
 QY 661 TCTCCGAGACTACCGGCTGCTTACTCCGCGGATGGTGGCGCTGGATGGGCTGGAGG 720
 Db 482 TCTCCGAGACTACCGGCTGCTTACTCCGCGGATGGTGGCGCTGGATGGGCTGGAGG 541
 QY 721 ACCGCTGGGCTCAGAGAGTATCTCAGGCAATGAGACCTGAGAGAGTGGTGGAGG 780
 Db 542 ACCGCTGGGCTCAGAGAGTATCTCAGGCAATGAGACCTGAGAGAGTGGTGGAGG 601
 QY 781 ACCTTGGGGCCCCCAATGTTGCCGACGTGGCTTACCCCGGGGCTGACCGGGTCA 840
 Db 602 ACCTTGGGGCCCCCAATGTTGCCGACGTGGCTTACCCCGGGGCTGACCGGGTCA 661
 QY 841 TGAATGCTGTCTGGGGGTAGAGTCTATGGCTGCTGAGAGGAGTGGAGTGGTCTGCTT 900
 Db 662 TGAATGCTGTCTGGGGGTAGAGTCTATGGCTGCTGAGAGGAGTGGAGTGGTCTGCTT 721
 QY 901 ACAACGCGCTGTGGGGCAGACATGATTTATCTGAGGCTGTACTTAAAGATCTCA 960
 Db 722 ACAACGCGCTGTGGGGCAGACATGATTTATCTGAGGCTGTACTTAAAGATCTCA 781
 QY 961 CCATATACGACATATACCGTGGGGGAGTGCAGATATGGGGCTGGGGCAGCTGGCAGATG 1020
 Db 782 CCATATACGACATATACCGTGGGGGAGTGCAGATATGGGGCTGGGGCAGCTGGCAGATG 841
 QY 1021 GTGTGGTGGGGCTGATGATCTTAAAGAGTGAAGAGTGGGGCTGGGGCTGGGGCTGATG 1080
 Db 842 GTGTGGTGGGGCTGATGATCTTAAAGAGTGAAGAGTGGGGCTGGGGCTGGGGCTGATG 901
 QY 1081 ACTATGTGGAGTGAACACACAGCTTCTCCAGTGGCTATGTGAGATGAGATTTAGT 1140
 Db 902 ACTATGTGGAGTGAACACACAGCTTCTCCAGTGGCTATGTGAGATGAGATTTAGT 961
 QY 1141 TTGACCGGCTGAGAGGCTTCCAGGCTATGCAAGTCCACTGTAAACAATGACACAGCTGG 1200
 Db 962 TTGACCGGCTGAGAGGCTTCCAGGCTATGCAAGTCCACTGTAAACAATGACACAGCTGG 1021
 QY 1201 GAGCCGCTGACCTGGCGGGGTGGAGTGTGCTTCCGGGGTGGGGCTGGCGCTGGAGCTGGG 1260
 Db 1022 GAGCCGCTGACCTGGCGGGGTGGAGTGTGCTTCCGGGGTGGGGCTGGCGCTGGAGCTGGG 1081
 QY 1261 AAGGGAGGACCAATGCGCCACAACCTAGGGGCAACCTGGGGGACCCCAAGAGCCGGGGCTG 1320
 Db 1082 AAGGGAGGACCAATGCGCCACAACCTAGGGGCAACCTGGGGGACCCCAAGAGCCGGGGCTG 1141
 QY 1321 TCTCAGTGGCTTGGCGGGCTGTGGCTGCTTCTGCAAGTGGCGCTTCTCTTTGGCG 1380
 Db 1142 TCTCAGTGGCTTGGCGGGCTGTGGCTGCTTCTGCAAGTGGCGCTTCTCTTTGGCG 1201
 QY 1381 GGCCTGCTTACTCTCAGCGAAATCTCTTCAATCTGATGTGGTGAACAATTTCTCTC 1440
 Db 1202 GGCCTGCTTACTCTCAGCGAAATCTCTTCAATCTGATGTGGTGAACAATTTCTCTC 1261
 QY 1441 CGGCACTGGAGGACACTTCCGCGAGCCCTGTGTGGCGGCTGGCCCACTCCACCA 1500
 Db 1262 CGGCACTGGAGGACACTTCCGCGAGCCCTGTGTGGCGGCTGGCCCACTCCACCA 1321

QY 1501 ACTTCAGACAGTGTGAGCTGAGCCAGAGGCGCAGAGCCGCTGGCCAGAGCGAGGGA 1560
 Db 1322 ACTTCAGACAGTGTGAGCTGAGCCAGAGGCGCAGAGCCGCTGGCCAGAGCGAGGGA 1381
 QY 1561 GCCGAGCCGCTATCTCATGCGGCTGCTGTGGCCATCATCTCTCTCTGCTCATCA 1620
 Db 1382 GCCGAGCCGCTATCTCATGCGGCTGCTGTGGCCATCATCTCTCTCTGCTCATCA 1441
 QY 1621 TTGCTCATGCTGTGGCGGGTGCACATGGGCGCAGGCTCTTCAGAAAGCTTAACAGGAGG 1680
 Db 1442 TTGCTCATGCTGTGGCGGGTGCACATGGGCGCAGGCTCTTCAGAAAGCTTAACAGGAGG 1501
 QY 1681 TGTGGAAGAGAGACTAGAGGTTACCTCTCTCTCTGGGAGCACTATCTCATCA 1740
 Db 1502 TGTGGAAGAGAGACTAGAGGTTACCTCTCTCTCTGGGAGCACTATCTCATCA 1561
 QY 1741 ACCGCCCAAGTCTCAGAGAGCCACCCCGTACAGAGAGCCCGGCTGTGGAAATCCG 1800
 Db 1562 ACCGCCCAAGTCTCAGAGAGCCACCCCGTACAGAGAGCCCGGCTGTGGAAATCCG 1621
 QY 1801 CCCACCTCGGCTCCCTGTGTCCTCCATGCTGTGGTGTCTCTCCATATCCAGCTTACC 1860
 Db 1622 CCCACCTCGGCTCCCTGTGTCCTCCATGCTGTGGTGTCTCTCCATATCCAGCTTACC 1681
 QY 1861 GCTTCCTTCTGCGCACTTACGCGCGTCCCGCTCGAGAGCCGCGGCGCCACACCGGCT 1920
 Db 1682 GCTTCCTTCTGCGCACTTACGCGCGTCCCGCTCGAGAGCCGCGGCGCCACACCGGCT 1741
 QY 1921 GGGCCAAACCCACACACCCAGGCTTACAGTGGGAGCTATATGAGAGCTGAGAGCCAG 1980
 Db 1742 GGGCCAAACCCACACACCCAGGCTTACAGTGGGAGCTATATGAGAGCTGAGAGCCAG 1801
 QY 1981 GCGGCGCGCTTCTGCGCCCACTCCCGCAGAAAGCGTCCCGCATATAGCCGAGCTACA 2040
 Db 1802 GCGGCGCGCTTCTGCGCCCACTCCCGCAGAAAGCGTCCCGCATATAGCCGAGCTACA 1861
 QY 2041 TTGTACCTCAGAGGCGTACCGGGGCAACACCTATGCTGTGCTGCACTGGCCCGAG 2100
 Db 1862 TTGTACCTCAGAGGCGTACCGGGGCAACACCTATGCTGTGCTGCACTGGCCCGAG 1921
 QY 2101 GGGCAGTGGGGAGTGGGCCCCCAGAGTGGATTTCCCTGATCTGACCTCGCTTCAAG 2160
 Db 1922 GGGCAGTGGGGAGTGGGCCCCCAGAGTGGATTTCCCTGATCTGACCTCGCTTCAAG 1981
 QY 2161 AGAAGCTGGCGAGGGGCAAGTGGGAGGTGCACTGTGTGAGGTGCAAGCCCTCAAG 2220
 Db 1982 AGAAGCTGGCGAGGGGCAAGTGGGAGGTGCACTGTGTGAGGTGCAAGCCCTCAAG 2041
 QY 2221 ATCTGTCAAGTCTTGAATTTCCCTTAATGTGGTAAGGAGACCTTGTGGTACTG 2280
 Db 2042 ATCTGTCAAGTCTTGAATTTCCCTTAATGTGGTAAGGAGACCTTGTGGTACTG 2101
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 QY 2341 ATTTCTGAAGAGTGAAGATATGTCAGAGGCTCAAGAGCCCAATATTTGGCTGC 2400
 Db 2144 ATTTCTGAAGAGTGAAGATATGTCAGAGGCTCAAGAGCCCAATATTTGGCTGC 2203
 QY 2401 TGGGCTGTGTGTCAGAGAGACCCCTGTCAGATTTACTGACTCATGAGAAAGGCG 2460
 Db 2204 TGGGCTGTGTGTCAGAGAGACCCCTGTCAGATTTACTGACTCATGAGAAAGGCG 2263
 QY 2461 ACCTCAACAGTCTCTCACTGCGCACAGCTGAGAGACAAGGAGCCGAGGGGCGCTG 2520
 Db 2264 ACCTCAACAGTCTCTCACTGCGCACAGCTGAGAGACAAGGAGCCGAGGGGCGCTG 2323
 QY 2521 GGGAGGAGAGGCTGGGAGGCGGCGCAACATAGCTATCCCAATGCTGTGATGTGGAG 2580
 Db 2324 GGGAGGAGAGGCTGGGAGGCGGCGCAACATAGCTATCCCAATGCTGTGATGTGGAG 2383

QY	2581	CCGAGATGCGCCCGGCAAGCGCCATATCTGCGCCACACTCAACTTCTTACATGCGGACCTGG	2640	
Db	2384	CCGAGATGCGCCCGGCAAGCGCCATATCTGCGCCACACTCAACTTCTTACATGCGGACCTGG	2443	
QY	2641	CCACGGGGAACCTGCTAGTTGGGGAAAAATTTCACATGAAAAATGCGACACTTTGGCATA	2700	
Db	2444	CCACGGGGAACCTGCTAGTTGGGGAAAAATTTCACATGAAAAATGCGACACTTTGGCATA	2503	
QY	2701	GCCGGAACCTGTATGCTGGGGGACTATTAACGCTGTGCAGAGCGCGGACAGTGTGCCATCC	2766	
Db	2504	GCCGGAACCTGTATGCTGGGGGACTATTAACGCTGTGCAGAGCGCGGACAGTGTGCCATCC	2563	
QY	2761	GCTGGATGGCCCGGGGAGTGCATCCCTCATGGGGAACTTACGACTGCGAGTACGTGTGGG	2820	
Db	2564	GCTGGATGGCCCGGGGAGTGCATCCCTCATGGGGAACTTACGACTGCGAGTACGTGTGGG	2623	
QY	2821	CCCTTGCTGTGACCCCTGTGGAGGTGCTGATGCTGTGAAGGCCACGCGCTTTGGGACG	2880	
Db	2624	CCCTTGCTGTGACCCCTGTGGAGGTGCTGATGCTGTGAAGGCCACGCGCTTTGGGACG	2683	
QY	2881	TCACCGACGACGAGTTCATTCGAAAGCGGGGGAGTTCTTCGGGAGACGAGCGCGGACG	2940	
Db	2684	TCACCGACGACGAGTTCATTCGAAAGCGGGGGAGTTCTTCGGGAGACGAGCGCGGACG	2743	
QY	2941	TGTACCTTCCCGCGCGCGCTGCCCTGCGCGGAGGCGCTATATGACCTGATGCTTGGTCT	3000	
Db	2744	TGTACCTTCCCGCGCGCGCTGCCCTGCGCGGAGGCGCTATATGACCTGATGCTTGGTCT	2803	
QY	3001	GGAGCCGGGAGTCTGAGCAGGAGCACACCTTTCCACGCTGCATCGGCTTCCTGGCAGAG	3060	
Db	2804	GGAGCCGGGAGTCTGAGCAGGAGCACACCTTTCCACGCTGCATCGGCTTCCTGGCAGAG	2863	
QY	3061	ATGCACTCAACACGGTGTGAATTCACACATTCAGCTGCCGCCCTCCCTCAAGGAGTATGAC	3120	
Db	2864	ATGCACTCAACACGGTGTGAATTCACACATTCAGCTGCCGCCCTCCCTCAAGGAGTATGAC	2923	
QY	3121	GGGAAGCCAGAGACACTTAAACAAGAGAGACAAATGCACTCTG - CCCTTCCCTCCCG	3179	
Db	2924	GGGAAGCCAGAGACACTTAAACAAGAGAGACAAATGCACTCTG - CCCTTCCCTCCCG	2983	
QY	3180	ACAGCCCATCACTCTATATAGAGGACGTGAGACTGACGAGTGGGGGTGGGCCACCCAGGGA	3239	
Db	2984	ACAGCCCATCACTCTATATAGAGGACGTGAGACTGAGACTGCA - ---GGTGGGCCACCCAGGGA	3039	
QY	3240	GCTGATGCCCTTCTCCCTTCTGAGACACTTCATGTCCTCCCTTCTGCTTCCTTC	3299	
Db	3040	GCTGATGCCCTTCTCCCTTCTGAGACACTTCATGTCCTCCCTTCTGCTTCCTTC	3099	
QY	3300	CTAGAAGCCCTCTGCGGCCACCCACGAGTGGTCTGTGATGGGATCCTCTCCACCCCTTC	3359	
Db	3100	CTAGAAGCCCTCTGCGGCCACCCACGAGTGGTGTGATGGGATCCTCTCCACCCCTTC	3159	
QY	3360	TAGCCATCCCTTGGGGAGAGGTGGGGAGAAATATAGGATATGACACTGAGACATGGGCCATT	3419	
Db	3160	TAGCCATCCCTTGGGGAGAGGTGGGGAGAAATATAGGATATGACACTGAGACATGGGCCATT	3219	
QY	3420	GGAGCACCCTGGGCCCACTGGAACAACCTGATTCCTGAGACAGGTGGCTGGC - CCCCAGCT	3478	
Db	3220	GGAGCACCCTGGGCCCACTGGAACAACCTGATTCCTGAGACAGGTGGCTGGC - CCCCAGCT	3279	
QY	3479	TCTTCTCCCTGTGCACACATGGAAACCCCACTGGCTAGAAATCTGGGGGTGAGAGAGCAA	3538	
Db	3280	TCTTCTCCCTGTGCACACATGGAAACCCCACTGGCTAGAAATCTGGGGGTGAGAGAGCAA	3339	
QY	3539	GAAAGAGAGAAATATGTTCTTGTGCTGCTGCTGCTGTACTGTGCTCCACACTTGGGGTCT	3598	
Db	3340	GAAAGAGAGAAATATGTTCTTGTGCTGCTGCTGCTGTACTGTGCTCCACACTTGGGGTCT	3399	
QY	3599	TCTTCTCCCTGTGCACACTGGAACCTGGAACCTGGGGGTAGCCCGGCCACCCCTCACTCA - 3657		
Db	3400	TCTTCTCCCTGTGCACACTGGAACCTGGAACCTGGGGGTAGCCCGGCCACCCCTCACTCA - 3459		
QY	3658	CCCCCACTTCCCACTGCAAGTCTGTAGCTAGAAACTTCTCTAAGCCTATACGTTTCTGTG	3717	

Db	3460	CCCCACATCCCACTGCAGTCTTGTAAGTAACCTTCNAAAGCCTACGTTCTCTG	3519
QY	3718	GAGTAAATATTTGGATTTGGGGGGAAGAAGGAGCAACGCCATACGCTTGGGGTGGAC	3777
Db	3520	GAGTAAATATTTGGATTTGGGGGGAAGAAGGAGCAACGCCATACGCTTGGGGTGGAC	3579
QY	3778	ATCTTAATGTAAGCTGCCACATGATTTTCTATATATCATGCTGGGGTTGTACATTTTGG	3837
Db	3580	ATCTTAATGTAAGCTGCCACATGATTTTCTATATATCATGCTGGGGTTGTACATTTTGG	3638
QY	3838	GGGGGAGAGACACAGATTTTTCACATAATATATGAGCACTAGCTTAGCAATTTTAAATCC	3897
Db	3639	GGGGGAGAGACACAGATTTTTCACATAATATATGAGCACTAGCTTAGCAATTTTAAATCC	3658
QY	3898	CCTGCATAGGAGAGTATATATTAAGTTGAGTTTCCACAAAAAATTTAAAAA	3950
Db	3699	CCTGCATAGGAGAGTATATATTAAGTTGAGTTTCCACAAAAAATTTAAAAA	3751

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RESULT 2
US-10-060-036-4549
; Sequence 4549; Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060, 036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4549
; LENGTH: 3849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4549

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Query Match	91.2%	Score 3613.4	DB 9	Length 3849
Best Local Similarity	95.9%	Pred. No. 0		
Matches 3792	Conservative 0	Mismatches 31	Indels 130	Gaps 3
QY	2	GAGCCTGAGACTGAGGGGTGACTGGAGCCTAAGAGAAATCCTGACACTGGAAGCCCCCGACACAC	61	
DB	24	GAGCCTGAGACGGGACTGCAAGCAGCCCCCTGGGGGGCCAGCTTTGAGAGCCCCCGACACAC	83	
QY	62	TGCTCTCGAGAGACCCGCTCCCGACACACCGAGGCCCGCCGCGGCGCTCCCGGCTCCGGGGTCC	121	
DB	84	TGCTCTCGAGAGACCCGCTCCCGACACACCGAGGCCCGCCGCGGCGCTCCCGGCTCCGGGGTCC	143	
QY	122	GCGGCTCTGGCTCCCTCCGCGCTCCCGCCGCTCCGCGCCGCGCGCGAGAGAGGCCCGCGCTC	181	
DB	144	GCGGCTCTGGCTCCCTCCGCGCTCCCGCCGCTCCGCGCCGCGCGAGAGAGGCCCGCGCTC	203	
QY	182	CCGGGTCCGAGAGCGCTTGGGTCTGCGCGGAAAGACGATGAGAGGTGTCTGAAGGTGGCTATT	241	
DB	204	CCGGGTCCGAGAGCGCTTGGGTCTGCGCGGAAAGACGATGAGAGGTGTCTGAAGGTGGCTATT	263	
QY	242	CACGTAGAGGATGGGGTTGGACTGTGAAGAAATGCCAAGATGCTGCCCCACCCCTTAG	301	
DB	264	CACGTAGAGGATGGGGTTGGACTGTGAAGAAATGCCAAGATGCTGCCCCACCCCTTAG	323	
QY	302	GCCGAGAGGATCAGAGAGCTATGGGACAGAGAGCCCTGCACTTATCTTACGCTGCTCTTT	361	
DB	324	GCCGAGAGGATCAGAGAGCTATGGGACAGAGAGCCCTGCACTTATCTTACGCTGCTCTTT	383	
QY	362	GGTGGCAAGTGGAGATGCTGACATGAAAGAGACATTTTATCCTGCGCAAGTCCCGCTATGC	421	

Db 384 GGTGCAAGTGAATGCTGACATGAGAGGACATTTGATCTGCAAGTCCCGTATGC 443
 Oy 422 CTTGGGCAATGAGAGACCGGACCATCCAGACATGATCTGCTTCCAGCTCTGTC 481
 Db 444 CTTGGGCAATGAGAGACCGGACCATCCAGACATGATCTGCTTCCAGCTCTGTC 503
 Oy 482 AGATTCACCTCCCGCCGACAGAGATTTGAGAGACATGACGGGATGGGGCTGTG 541
 Db 504 AGATTCACCTCCCGCCGACAGAGATTTGAGAGACATGACGGGATGGGGCTGTG 563
 Oy 542 CCGGCAAGGCTGGGATTTCCAGAGAGAGAGATCTGAGGTGATCTACACAGCT 601
 Db 564 CCGGCAAGGCTGGGATTTCCAGAGAGAGAGATCTGAGGTGATCTACACAGCT 623
 Oy 602 CCACCTGGTGGCTGTGTGACACCCAGAGGACATGCCGGGGGCTGGGCAAGAGAT 661
 Db 624 GCACCTGGTGGCTGTGTGACACCCAGAGGACATGCCGGGGGCTGGGCAAGAGAT 683
 Oy 662 CTCCCGAGCTACCGGCTGCTTACTCCCGGAGATGGTGGCTGGATGGGCTGGAAGA 721
 Db 684 CTCCCGAGCTACCGGCTGCTTACTCCCGGAGATGGTGGCTGGATGGGCTGGAAGA 743
 Oy 722 CCGGTCGGGTCAGAGAGATCTAGAGCAATGAGAGACCTGAGGAGATGGTGGTGAAGA 781
 Db 744 CCGGTCGGGTCAGAGAGATCTAGAGCAATGAGAGACCTGAGGAGATGGTGGTGAAGA 803
 Oy 782 CTTGGGACCCGCAATGCTGACCTGCTTACCCCGGGGCTGACCGGCTCAT 841
 Db 804 CTTGGGACCCGCAATGCTGACCTGCTTACCCCGGGGCTGACCGGCTCAT 863
 Oy 842 GAGTGTCTGTCTGCGGGTAGAGCTATAGCTGCTGCTGAGAGGATGAGATCTGTCTTA 901
 Db 864 GAGTGTCTGTCTGCGGGTAGAGCTATAGCTGCTGCTGAGAGGATGAGATCTGTCTTA 923
 Oy 902 CACGCGCCCTGTGGGGAGAGCAATGATTTATCTGAGCGGCTGATCTCAACGACTCAC 961
 Db 924 CACGCGCCCTGTGGGGAGAGCAATGATTTATCTGAGCGGCTGATCTCAACGACTCAC 983
 Oy 962 CTATGAGGACATACCTGCGGAGCTGACATGAGTGGGGGCTGGGGAGCTGAGATGG 1021
 Db 984 CTATGAGGACATACCTGCGGAGCTGACATGAGTGGGGGCTGGGGAGCTGAGATGG 1043
 Oy 1022 TGTGTGTGGGCTGATATCTTTAGAGAGATGACAGACCTGGGGCTTGGCCAGCTATGA 1081
 Db 1044 TGTGTGTGGGCTGATATCTTTAGAGAGATGACAGACCTGGGGCTTGGCCAGCTATGA 1103
 Oy 1082 CTATGAGGACATACCTGCGGAGCTGACATGAGTGGGGGCTGGGGAGCTGAGATGG 1141
 Db 1104 CTATGAGGACATACCTGCGGAGCTGACATGAGTGGGGGCTGGGGAGCTGAGATGG 1163
 Oy 1142 TGACCGGCTAGAGGCTTCCAGAGCTATGACAGTCCACTGTAAACATGACAGAGCTGGG 1201
 Db 1164 TGACCGGCTAGAGGCTTCCAGAGCTATGACAGTCCACTGTAAACATGACAGAGCTGGG 1223
 Oy 1202 AGCCCGCTGTGCTGGGCGGCTGAGATGCTTCCCGGCTGGGCTGAGGCTGGGA 1261
 Db 1224 AGCCCGCTGTGCTGGGCGGCTGAGATGCTTCCCGGCTGGGCTGAGGCTGGGA 1283
 Oy 1262 GGGGAGGACCATGGGAGCAACCACTAGGGGAGCAACCTGGGGAGACCCGAGAGCCGGGCTGT 1321
 Db 1284 GGGGAGGACCATGGGAGCAACCACTAGGGGAGCAACCTGGGGAGACCCGAGAGCCGGGCTGT 1343
 Oy 1322 CTGAGTGGCCCTTGGGCGGCTGTGCTGCTTCTGACATGAGCGGCTTCTCTTTGGGG 1381
 Db 1344 CTGAGTGGCCCTTGGGCGGCTGTGCTGCTTCTGACATGAGCGGCTTCTCTTTGGGG 1403
 Oy 1382 GCGCTGTACTCTTACAGGAATCTCTTCATCTGTGATGGTGAACAAATCTCTCC 1441
 Db 1404 GCGCTGTACTCTTACAGGAATCTCTTCATCTGTGATGGTGAACAAATCTCTCC 1463
 Oy 1442 GCGCTGTGGAGGACCTTCCGCGAGCCGCTGTGGCGGCTGGGCCACCTCCACCA 1501

Db 1464 GGCACGTGGAGGACCTTCCCGCAGCCGCTGTGGGCGGCTGGGCCACCTCCACCA 1523
 Oy 1502 CTTGAGAGCTTGGAGCTGAGGCGCAGAGGCGGAGGCGGCTGGGCAAGGCGGAGG 1561
 Db 1524 CTTGAGAGCTTGGAGCTGAGGCGCAGAGGCGGAGGCGGCTGGGCAAGGCGGAGG 1583
 Oy 1562 CCGGACCGCATCTCATGAGCTGCTGTGGGCTGAGGCTGCTGCTGCTCATCAT 1621
 Db 1584 CCGGACCGCATCTCATGAGCTGCTGTGGGCTGAGGCTGCTGCTGCTCATCAT 1643
 Oy 1622 TGCCCTATGCTGTGGGCGCTGACACTGGCGAGGCTCTCAAGAGGCTGAAGAGG 1681
 Db 1644 TGCCCTATGCTGTGGGCGCTGACACTGGCGAGGCTCTCAAGAGGCTGAAGAGG 1703
 Oy 1682 GTTGAAGAGAGGCTGAGAGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
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 Oy 1742 CCGGCAAGGCTGAGAGGAGCCGCTTACAGAGGAGCCGCGGCTGCTGCTGCTGCT 1801
 Db 1764 CCGGCAAGGCTGAGAGGAGCCGCTTACAGAGGAGCCGCGGCTGCTGCTGCTGCT 1823
 Oy 1802 CCACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1861
 Db 1824 CCACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1884
 Oy 1862 CCTCTTGTGGCACTTACGCGGCTCCCGCTGAGGCGGCGGCGGCGGCGGCGGCT 1921
 Db 1884 CCTCTTGTGGCACTTACGCGGCTCCCGCTGAGGCGGCGGCGGCGGCGGCGGCT 1941
 Oy 1922 GGCACCAACCCACCAACCCAGGCTACAGTGGGGAGCTATATGAGGCTGAGAGCCAG 1981
 Db 1944 GGCACCAACCCACCAACCCAGGCTACAGTGGGGAGCTATATGAGGCTGAGAGCCAG 1999
 Oy 1982 GCGCGGCTTGTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2041
 Db 1999 GCGCGGCTTGTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2061
 Oy 2042 TGTACCTGAGAGGCGCTGACCGGGGAGCAACCTATGCTGCTGCTGCTGCTGCTGCT 2101
 Db 2061 TGTACCTGAGAGGCGCTGACCGGGGAGCAACCTATGCTGCTGCTGCTGCTGCTGCT 2121
 Oy 2102 GGCAGTGGGAGTGGGCGGCGGCTGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCT 2161
 Db 2121 GGCAGTGGGAGTGGGCGGCGGCTGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCT 2181
 Oy 2162 GAGGCTTGGGAGGCGGCTGAGTGGGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCT 2221
 Db 2181 GAGGCTTGGGAGGCGGCTGAGTGGGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCT 2241
 Oy 2222 TGTGCTGAGTGGATTTCCCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2281
 Db 2241 TGTGCTGAGTGGATTTCCCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2301
 Oy 2282 CAAGATCTTACGGGAGGCTGAGTGGGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCT 2341
 Db 2301 CAAGATCTTACGGGAGGCTGAGTGGGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCT 2361
 Oy 2342 TTTCTTAAAGAGGCTGAGTGGGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2401
 Db 2361 TTTCTTAAAGAGGCTGAGTGGGAGTGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2421
 Oy 2402 GGGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2461
 Db 2421 GGGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2481
 Oy 2462 CTTCAACCACTTCTCATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2521
 Db 2481 CTTCAACCACTTCTCATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2541
 Oy 2522 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2581
 Db 2541 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2601

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QY 2532 CCAGATCGCTCCGGGCGATGCGCTATCTGGCCACACTCACTTTGATACATCGGGAGCTGAC 2641
DB 2475 CCAGATCGCTCCGGGCGATGCGCTATCTGGCCACACTCACTTTGATACATCGGGAGCTGAC 2534
QY 2662 CACGGGAAATGCTGATGTTGGGAAATTTACACATCAAAATCGACAGATTTGGCATGAG 2701
DB 2535 CACGGGAAATGCTGATGTTGGGAAATTTACACATCAAAATCGACAGATTTGGCATGAG 2594
QY 2702 CCGGAACCTCTATGCTGGGAGTATTAACGCTGAGGGCCGGGAGTGGCTCCATCCG 2761
DB 2595 CCGGAACCTCTATGCTGGGAGTATTAACGCTGAGGGCCGGGAGTGGCTCCATCCG 2654
QY 2762 CTGATGAGCTGGGAGTGCATCTTCATGAGGAAATTCACGACTGGAGTGCATGAGG 2821
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DB 2715 CTTGATGATGACCTGCTGGGAGTGCATGCTCTGTAGGGCCGACCCCTTTGGGAGCT 2774
QY 2882 CACGAGAGGAGGATCGAAGAAAGCGGGGAGTCTCCGGGACGACGGCCGACAGT 2941
DB 2775 CACGAGAGGAGGATCGAAGAAAGCGGGGAGTCTCCGGGACGACGGCCGACAGT 2834
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DB 2835 GTACCTGTCCCGGCGCTGCTGCTGCGCCAGAGGCTTATGATGATGATGATGATG 2894
QY 3002 GAGCCGGGAGTCTGAGACGACGACACCCCTTTCCAGCTGATGCTGCTGAGAGGA 3061
DB 2895 GAGCCGGGAGTCTGAGACGACGACACCCCTTTCCAGCTGATGCTGCTGAGAGGA 2954
QY 3062 TGCACTCAACAGGCTGTAATACACATCCAGCTGCTGCTGAGAGGATGATGAG 3121
DB 2955 TGCACTCAACAGGCTGTAATACACATCCAGCTGCTGCTGAGAGGATGATGAG 3014
QY 3122 GGAAGCCAGTGCATCAAAACAGAGGACATGAGGACCTGCTGCTGCTGCTGCTG 3181
DB 3015 GGAAGCCAGTGCATCAAAACAGAGGACATGAGGACCTGCTGCTGCTGCTGCTG 3074
QY 3182 AGCCCATCACCCTTAATAGAGGACAGTGCAGAGTGGGCTGGGCCACACAGGAGG 3241
DB 3075 AGCCCATCACCCTTAATAGAGGACAGTGCAGAGTGGGCTGGGCCACACAGGAGG 3134
QY 3242 TGATGCCCTTCTCCCTCTCTGAGACACACTGATGCTGCTGCTGCTGCTGCTG 3301
DB 3135 TGATGCCCTTCTCCCTCTCTGAGACACACTGATGCTGCTGCTGCTGCTGCTG 3184
QY 3302 AGAAGCCCTGTGCGCCACCCAGCTGCTGCTGATGGAGTCTGCTGCTGCTGCTG 3361
DB 3195 AGAAGCCCTGTGCGCCACCCAGCTGCTGCTGATGGAGTCTGCTGCTGCTGCTG 3254
QY 3362 GCCATCCCTTGGGGAAGGTTGGGGAATAATAGATAGACATGACATGGCCATGG 3421
DB 3255 GCCATCCCTTGGGGAAGGTTGGGGAATAATAGATAGACATGACATGGCCATGG 3314
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QY 3481 TCTCTCCCTGTACACACTGAGACCCCACTGCTGAGATCTGGGGGAGAGAGACAAGA 3540
DB 3375 TCTCTCCCTGTACACACTGAGACCCCACTGCTGAGATCTGGGGGAGAGAGACAAGA 3434
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DB 3495 CTCTCTCATCTGAGAAACAGTGCAGTGGGGGAGAGCCCGCCACCTGATGACACC 3554

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QY 3661 CCACCTCCACTTGGAGTCTGATGTAAGTAATCTCTAAGCTATAGCTTTCTGGAG 3720
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QY 3841 GGAGAGACACAGATTTTACACTAATATATGAGTACTGATGAGCAATTTTATCCCT 3900
DB 3735 GGAGAGACACAGATTTTACACTAATATATGAGTACTGATGAGCAATTTTATCCCT 3794
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RESULT 3

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US-09-223-490-3
; Sequence 3, Application US/09223490
; Patent No. US20020147325A1

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GENERAL INFORMATION:

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APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/223,490
FILING DATE:

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CLASSIFICATION:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170,558
FILING DATE:

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ATTORNEY/AGENT INFORMATION:

```

NAME: Haasak, Janet E. 28,616
REGISTRATION NUMBER: 854C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3637 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-223-490-3

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Query Match

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Best Local Similarity 87.1%; Score 3451; DB 10; Length 3637;
Pred. No. 0;
Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;

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Qy 496 CCCGCCACAGCAGGTGGAGAGCAGTGAACGGGAGTGGGAGCTGGTGGCCCGCAGAGGTCGG 555
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Db 257 CCGGCCACAGAGAGTGGAGAGCAGTGAACGGGAGTGGGAGCTGGTGGCCCGCAGAGGTCGG 316
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Db 317 TGTTCCTCCAGAGAGAGAGTACTGCAAGTGGATCTACACAGACTCCACCTGGTGGCTC 376
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Qy 616 TGTGGGCAACCCAGAGAGAGTACCGGGGGCCCTGGGCAAGAGATTTCTCCGGAGCTACC 675
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Db 437 GCGTGCCTTACTCCCGGGAGATGTCGCGCTGATGGGCTGGAGAGACCGCTGGGGTCAAG 496
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Qy 2416 AGGACGACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2475
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DB 2279 GCGAGGGGCCCCACATCAGCTACCCATCTCTGCTGATGTGGAGCCCAAGATGCTCCG 2338
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DB 2973 CCCACCCAGCTGTCCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3032
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QY 3436 ACTGAGACACACTGATCTCTGAGAGAGTGGCTGGC-CCCGAGCTTCTCTCTCTCTCTCTCTCT 3494
DB 3093 ACTGAGACACACTGATCTCTGAGAGAGTGGCTGGC-CCCGAGCTTCTCTCTCTCTCTCTCTCT 3152
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DB 3153 ACATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3212

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QY 3555 TTTCCCTGAGCGTGCCTGCTGATCTGTCTCTCAGCTTGGGCTTCTCTCTCTCTCTCTCT 3614
DB 3213 TTTCCCTGAGCGTGCCTGCTGATCTGTCTCTCAGCTTGGGCTTCTCTCTCTCTCTCTCT 3272
QY 3615 GAACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3674
DB 3273 GAACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3332
QY 3675 CAGCTCTGAGTGAAGACTTCTCTAAGCCTTAACCTTTCTGTGAGATAAATTTGGAGT 3734
DB 3333 CAGCTCTGAGTGAAGACTTCTCTAAGCCTTAACCTTTCTGTGAGATAAATTTGGAGT 3392
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DB 3393 GGGGGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3452
QY 3795 CACATTTGATTTTCTATATATGACCTTGGGCTTGTACATTTTGGGGGAGAGACAGAT 3854
DB 3453 CACATTTGATTTTCTATATATGACCTTGGGCTTGTACATTTTGGGGGAGAGACAGAT 3512
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RESULT 4

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US-09-925-297-279
Sequence 279, Application US/09925297
Patent No. US2002081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 279
LENGTH: 2861
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2861)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-279

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Query Match 70.3%; Score 2783.6; DB 10; Length 2861;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2833; Conservative 5; Mismatches 4; Indels 20; Gaps 3;

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QY 1093 GGACACACACAGCTTCTCCAGTGGCTATGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1152
DB 1 GGACACACACAGCTTCTCCAGTGGCTATGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 1153 GGGCCTTCCAGAGCTATGACGTCAGTGTAAACATGACAGCGTGGGAGCCCGCTGC 1212
DB 61 GGGCCTTCCAGAGCTATGACGTCAGTGTAAACATGACAGCGTGGGAGCCCGCTGC 120
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DB 121 CTGGCGGGGTGGAATGTGCTTCGCGGAGTGGCCCTGGCATGGCTGGGAGAGAGAGAGAGAG 180
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D	301	TTCTTACAGAAAT	TCCTTCACTCTATGTGGTAA	CAATTCCTTCCCGCACTGGAG	360	
Q	1453	GCACCTTCCGCGC	AGGCCCGCTGTGGGCGCGCTGGGCC	CACTCCACCAATTCAGACGT	1512	
D	361	GCACCTTCCGCGC	AGGCCCGCTGTGGGCGCGCTGGGCC	CACTCCACCAATTCAGACGT	420	
Q	1513	TGAGAGCTGGAG	CCCAAGGCCAGACCGCTGGCCAA	AGGCCGAGGGAGCCCGCAC	1572	
D	421	TGAGAGCTGGAG	CCCAAGGCCAGACCGCTGGCCAA	AGGCCGAGGGAGCCCGCAC	480	
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Q	1633	TCTGGCGGCTGC	ACATGGCGCGCTCTCAAGCAAGGCTGTA	AGGAGGTGTGGAAGG	1692	
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D	601	AGCTGACGGTTAC	CTCTGTCCCTGGGACACTATCTCATACAC	ACCGCCAGATC	660	
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D	661	CTAAGAGGCAAC	CCCGGCTACAGAGACCGCGGCTCGTGGGA	ATCCGCGCCCACTCCGCTC	720	
Q	1813	CGTGTGTCCCAAT	AGGCTGTGCGTGTGCTCTCAATCCAG	ACGCTTACCGGCTCTGTGG	1872	
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Q	1873	CCACTTACGGCG	CTCCCGCTGAGAGGCCCGGCGCCCCAC	ACCGGCTGTGGGCCAAACCA	1932	
D	781	CCACTTACGGCG	CTCCCGCTGAGAGGCCCGGCGCCCCAC	ACCGGCTGTGGGCCAAACCA	840	
Q	1933	CCAAACACCAAG	CGCTTAAGTGGGGACATATATGAGAGCTG	AGAGGCCAGGCGCCCGCTTC	1992	
D	841	CCAAACACCAAG	CGCTTAAGTGGGGACATATATGAGAGCTG	AGAGGCCAGGCGCCCGCTTC	900	
Q	1993	TGCCCCCACTCC	CCCAAGACAGCGTCCCGCATTAATGCGAG	GGCGGATATGTTACCTGC	2052	
D	901	TGCCCCCACTCC	CCCAAGACAGCGTCCCGCATTAATGCGAG	GGCGGATATGTTACCTGC	960	
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QY	2413	TGCAGAGACAGCCCTCTGCATGATTTACTGATGACTACATGAGAACGGGCACTCAACAGT	2417
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Db	1363	TCCTCAGTCCCAACAGCTGAGAGCAAGGACGCCGAGGGGGCCCTGGGGACGGGCAGG	1422
QY	2533	CTGGCCAGAGGGGCCCACTACAGCTCCCAATGCTGCTGCATGTGGCACCACAGATCGCTT	2592
Db	1433	CTGGCCAGAGGGGCCCACTACAGCTCCCAATGCTGCTGCATGTGGCACCACAGATCGCTT	1482
QY	2593	CCGGCATCGCTATCTGGCCACACTCACTTGTATCTACATCGGGACCTGGCCACGGCGAAT	2653
Db	1483	CCGGCATCGCTATCTGGCCACACTCACTTGTATCTACATCGGGACCTGGCCACGGCGAAT	1542
QY	2653	GCCATGTTGGGGAAAAATTTCACATCAAAATTCGACACTTTGGCATGTGACACCGCGAACCTCT	2712
Db	1533	GCCATGTTGGGGAAAAATTTCACATCAAAATTCGACACTTTGGCATGTGACACCGCGAACCTCT	1602
QY	2713	ATGCTGGGGAGATATTACCGTGTGCAGGGCCGGGAGTGTCTGCGCCATCCGCTGGATGGCTT	2772
Db	1603	ATGCTGGGGAGATATTACCGTGTGCAGGGCCGGGAGTGTCTGCGCCATCCGCTGGATGGCTT	1662
QY	2773	GGGAGTGCATCTCTCATGGGAAATTACAGACTCGGATGGATGTGTGGGCTTTGGTGTGA	2832
Db	1663	GGGAGTGCATCTCTCATGGGAAATTACAGACTCGGATGGATGTGTGGGCTTTGGTGTGA	1722
QY	2833	CCCGTGGGAGTGTGTATGCTGTGTAGGGGCCAGCCCTTTGGGAGAGTCAACGACAGC	2892
Db	1723	CCCGTGGGAGTGTGTATGCTGTGTAGGGGCCAGCCCTTTGGGAGAGTCAACGACAGC	1782
QY	2893	AGGTCTATGAGAACGGCGGGGAGTCTTCCGGAGACAGGGCCGGCAGGTGTACCTGTCTCC	2952
Db	1783	AGGTCTATGAGAACGGCGGGGAGTCTTCCGGAGACAGGGCCGGCAGGTGTACCTGTCTCC	1842
QY	2953	GGCGCGCTCTGCCCCCGAGGGCCATATGAGCTGTATCTTCGGTGTCTGTGAGCCGGGAGT	3012
Db	1843	GGCGCGCTCTGCCCCCGA -GGCYATATGTAGCTGTATCTTCGGTGTCTGTGAGCCGGGAGT	1901
QY	3013	CTGAGACAGCAGCAACCCCTTTCCGACGTGCACTCGGTTCTCTGGACAGAGATCACTCAACA	3072
Db	1902	CTGAGACAGCAGCAACCCCTTTCCGACGTGCACTCGGTTCTCTGGACAGAGATCACTCAACA	1961
QY	3073	CGGTGTGATTCACACATTCACAGCTGCCCTCCCTCAGAGGATGATCCAGGGAGGCACTG	3132
Db	1962	CGGTGTGATTCACACATTCACAGCTGCCCTCCCTCAGAGGATGATCCAGGGAGGCACTG	2021
QY	3133	ACACTAAAGACAAGGAGACACATGAGACACTGTGCGCTCCGCCCTCCGACACCCCATACAC	3192
Db	2022	ACACTAAAGACAAGGAGACACATGAGACACTGTGCGCTCCGCCCTCCGACACCCCATACAC	2081
QY	3193	TCTAATAGAGCAGTGAAGACTGACAGTGGGTGGGGCCACCCAGAGGAGACTATGCCCTT	3252
Db	2082	TCTAATAGAGCAGTGAAGACTGACAGTGGGTGGGGCCACCCAGAGGAGACTATGCCCTT	2141
QY	3253	CTCCGCTTCTCGAGACACTCTCATGTGCCCTTCTGTCTTCTTCTCTAGAGCCCTG	3312
Db	2142	CTCCGCTTCTCGAGACACTCTCATGTGCCCTTCTGTCTTCTTCTCTAGAGCCCTG	2201
QY	3313	TCGGCCACCCAGCTGTGCTGTGTGATGGGATCTCTCCACCCCTCTTAGGACATCCCTG	3372
Db	2202	TCGGCCACCCAGCTGTGCTGTGTGATGGGATCTCTCTCCACCCCTCTTAGGACATCCCTG	2261
QY	3373	GGGAGAGGTGGGGAAAAATATAGATAGACACTGAGATGGCCCATTTGGAGACACTGGGC	3432
Db	2262	GGGAGAGGTGGGGAAAAATATAGATAGACACTGAGATGGCCCATTTGGAGACACTGGGC	2321
QY	3433	CCCACTGGACAAACAGTATTCCTGTGAGAGGGGTGGG -CCCAAGCTTCTCTCCCTGT	3491
Db	2322	CCCACTGGACAAACAGTATTCCTGTGAGAGGGGTGGG -CCCAAGCTTCTCTCCCTGT	2381

OY	3492	CACACACTGAGCCCCCACTGGCTGAAATCTGGGGGTGAGGAGGACAAGAAGGAGAAA	3551
Db	2382	CACACACTGGAGCCCACTGGCTGGAATCTGGGGGTGAGGAGGACAAGAAGGAGAAA	2441
OY	3552	ATGTTCTTGTCGCTCCTCCTGTAATTGTCCTAGCTTGGGCTTCTTCCCTGCCATCA	3611
Db	2442	ATGTTCTTGTCGCTCCTCCTGTAATTGTCCTAGCTTGGGCTTCTTCCCTGCCATCA	2501
OY	3612	CCTAAACACTGGAGCTGGGGGTAGCCCGCCGACCCTCAGCACCCCACACTGCCAC	3671
Db	2502	CCTAAACACTGGAGCTGGGGGTAGCCCGCCGACCCTCAGCACCCCACACTGCCAC	2561
OY	3672	TTCGAGCTCTTGACTGAACTTCTTAAGCCTATACGTTTCTGTGAGATAAATATTTGG	3731
Db	2562	TTCGAGCTCTTGACTGAACTTCTTAAGCCTATACGTTTCTGTGAGATAAATATTTGG	2621
OY	3732	ATTGGGGGGAAGGAGGAGCACAAGGCCCATAGCCCTTGGGGGTGGACATCTCTAGTAGC	3791
Db	2622	ATTGGGGGGAAGGAGGAGCACAAGGCCCATAGCCCTTGGGGGTGGACATCTCTAGTAGC	2681
OY	3792	TGCCACATGATTTTTCTTAATATCACTTGGGGTTGTACATTTTTGGGGGAGAGACACA	3851
Db	2682	TGCCACATGATTTTTCTTAATATCACTTGGGGTTGTACATTTTTGGGGGAGAGACACA	2741
OY	3852	GATTTTACACTAATATATGAGACTACTGTAGAGCAATTTAATCCCTGCACATAGGCAG	3911
Db	2742	GATTTTACACTAATATATGAGACTACTGTAGAGCAATTTTAAATCCCTGCACATAGGCAG	2801
OY	3912	GTAATTAATAAAGGTGAGTTTCCACAAAAAATAAAAAAAAA	3953
Db	2802	GTAATTAATAAAGGTGAGTTTCCACAAAAAATAAAAAAAAA	2843

RESULT 5
US-09-223-490-7
Sequence 7, Application US/09223490
Patent No. US20020147325A1
GENERAL INFORMATION:
APPLICANT: Godowsk1, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/223,490
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170,558
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haseak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 854C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ. ID NO.: 7:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1197 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-223-490-7

Query Match      30.1%; Score 1192.2; DB 10; Length 1197;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1194; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY      375 GATGCTGACATGAGGAGACATTTTGATCTCGCCAACTGCGGTATGCCCTGGGCATGACG 434
Db      1 GATGCTGACATGAGGAGACATTTTGATCTCGCCAACTGCGGTATGCCCTGGGCATGACG 60

QY      435 GACCGGACCATCCGACAGCTGACATCTGCTCTCCAGTCCGCTATGCTCCCTGGGCATGACG 494
Db      61 GACCGGACCATCCGACAGCTGACATCTGCTCTCCAGTCCGCTATGCTCCCTGGGCATGACG 120

QY      495 GCCCGCCACAGCAGGTTGGAGAGCAGTGAACGGGGATGAGGGCTGTCGCCCGCAGAGTGC 554
Db      121 GCCCGCCACAGCAGGTTGGAGAGCAGTGAACGGGGATGAGGGCTGTCGCCCGCAGAGTGC 180

QY      555 GGTGTTCCCAAGGAGGAGAGTACTTGCAGGTGATCTTCAACAGACTCCACTGTGGCT 614
Db      181 GGTGTTCCCAAGGAGGAGAGTACTTGCAGGTGATCTTCAACAGACTCCACTGTGGCT 240

QY      615 CTGTGTGGGACACCCAGGAGACGGCATCCGGGGGCTGGGGCAAGAGTTCGCCGGAGCTAC 674
Db      241 CTGTGTGGGACACCCAGGAGACGGCATCCGGGGGCTGGGGCAAGAGTTCGCCGGAGCTAC 300

QY      675 CGGCTGCGTTACTCCCGGGATGGTCGCGCTGATGGGCTGGAAAGACCGCTGGGGTCAAG 734
Db      301 CGGCTGCGTTACTCCCGGGATGGTCGCGCTGATGGGCTGGAAAGACCGCTGGGGTCAAG 360

QY      735 GAGTGTGATCTCAAGGAATGAGGACCCCTAGAGGAGTGGTGCCTAAAGACTTGGGGCCCC 794
Db      361 GAGTGTGATCTCAAGGAATGAGGACCCCTAGAGGAGTGGTGCCTAAAGACTTGGGGCCCC 420

QY      795 ATGTTGGCCCGACTGTTCCGTTTCAACCCCGGCTGACCGGGTATGATAGTGTCTGTGCG 854
Db      421 ATGTTGGCCCGACTGTTCCGTTTCAACCCCGGCTGACCGGGTATGATAGTGTCTGTGCG 480

QY      855 CGGCTAAGAGCTCTAATGGCTGCTCTGAGAGGATGAGACTCTGTCTTCAACCGCCCTGTG 914
Db      481 CGGCTAAGAGCTCTAATGGCTGCTCTGAGAGGATGAGACTCTGTCTTCAACCGCCCTGTG 540

QY      915 GGGCGAACAATGATTTATCTGAGGCGGATGACCTCAACGACTCCACTATGAGCGGACAT 974
Db      541 GGGCGAACAATGATTTATCTGAGGCGGATGACCTCAACGACTCCACTATGAGCGGACAT 600

QY      975 ACCGTGGGCGACTGACATATGGGGGCTGTGGGCGAGCTGGGAGATGATGTGTGGGGCTG 1034
Db      601 ACCGTGGGCGAGCTGACATATGGGGGCTGTGGGCGAGCTGGGAGATGATGTGTGGGGCTG 660

QY      1035 GATACACTTAAGAAAGAGTCACAGAGCTGGGGGTCTGGCCAGGCTATGATATGTGGATGG 1094
Db      661 GATGACTTTAAGAAAGAGTCACAGAGCTGGGGGTCTGGCCAGGCTATGATATGTGGATGG 720

QY      1095 AGCAACACACACTTCTCCAGTGGGTATGTGAGATGAGATTGAGTTGACCGGCTGAGG 1154
Db      721 AGCAACACACACTTCTCCAGTGGGTATGTGAGATGAGATTGAGTTGACCGGCTGAGG 780

QY      1155 GCCTTCCAGGCTATGACAGGTCCACTGTAAACAATGACACACGCTGGGAGCCGCTGTGCT 1214
Db      781 GCCTTCCAGGCTATGACAGGTCCACTGTAAACAATGACACACGCTGGGAGCCGCTGTGCT 840

QY      1215 GGGGGGGGGAATATCGCTTCGGCGGGGCGGCTCCATAGGCTGGGAGGGGAGCCCATG 1274
Db      841 GGGGGGGGGAATATCGCTTCGGCGGGGCGGCTCCATAGGCTGGGAGGGGAGCCCATG 900

QY      1275 CGCCACAACCTTAGGGGGCAACTGGGGGACCCCAAGACCCGGGGCTGTCTCAGTCCGCTT 1334

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Query Match	Score	95% DB	Length	12010;
Best Local Similarity	89.7%	Pred.	1.5e-260;	
Matches 1139;	Conservative	0;	Mismatches 5;	Indels 126; Gaps 6;
QY	2789	GGGGAAGTTTCACGAGCTCGGAGTGTGGGCTTTGGTGTGACCTGTGGAGGTGCT	2848	
Db	10746	GGGGAAGTTTCACGAGCTCGGAGTGTGGGCTTTGGTGTGACCTGTGGAGGTGCT	10806	
QY	2849	GATGCTCTGTAGGGCCAGCCCTTTGGGAGGTCACCGAGCGAGCGATGATGAAACC	2908	
Db	10806	GATGCTCTGTAGGGCCAGCCCTTTGGGAGGTCACCGAGCGAGCGATGATGAAACC	10866	
QY	2909	GGGGAGTTCTTCCGGGACAGGGCCGC-----	2936	
Db	10866	GGGGAGTTCTTCCGGGACAGGGCCGCAGTGTGAGAGAGGAGGAAGATGGTTC	10922	
QY	2937	-----	2936	
Db	10926	CGAGNCGGGGGACAGAAAGGCGCAGACTTTCATCTTGGAGACTAAAGAAATTTGTTC	10986	
QY	2937	-----CAGGTGTACCTGTGTCCGGCCGCTGTGCTGCCGC	2970	
Db	10986	TGACTGTCAACACACATTCNCNCAATNCGAGGTGTACTGTGCCGGCCGCTGTGCTGCCGC	11045	

QY	2971	AGGGCCATATATAGACTATGCTTGGGAGCTGGAGCCGGAGATCTAGAGAGACACCT	3030
Db	11046	AGGGCCATATATAGACTATGCTTGGGAGCTGGAGCCGGAGATCTAGAGAGACACCT	111051
QY	3031	TTTCCAGCTGCATCGGTTCTCTGGCAGAGATGCACTAACACGGTGTGAATCAACATC	3090
Db	11106	TTTCCAGCTGCATCGGTTCTCTGGCAGAGATGCACTAACACGGTGTGAATCAACATC	111055
QY	3091	CACCTGCCCCCTCCCTCAGGGAGTATCCAGGGAGAACCCAGTACACTAAACAMAGAGNC	3150
Db	11166	CACCTGCCCCCTCCCTCAGGGAGTATCCAGGGAGAACCCAGTACACTAAACAMAGAGNC	112255
QY	3151	ACATGGACACCTGNG--CCCTTCCCCCTCCCGACACCCATCACTCTAATATAGAGCATGA	3209
Db	11226	ACATGGACACCTTGCCCCCTTCCCCCTCCCGACACCCCATCACTCTAATATAGAGCATGA	112855
QY	3210	GACTGCAGGTGGGCTGGGCCACCCAGAGAGCATGATGCCCTTCTCCCTCTCTGGACAC	3269
Db	11286	GACTGCA---GGCTGGGCCACCCAGAGAGCATGATGCCCTTCTCCCTCTCTGGACAC	113411
QY	3270	ACCTCTATGTCCTTCTCTGTTCTTCTCTCTCTAGAACCCCTGTGCCCCACACCTGCT	3329
Db	11342	ACCTCTATGTCCTTCTCTGTTCTTCTCTCTCTAGAACCCCTGTGCCCCACACCTGCT	114011
QY	3330	CCGTGGATGGGATCCCTCCACCCCTCTCTAGCAATCCCTTGGGGAGAGGCTGGGAGAA	3389
Db	11402	CCGTGGATGGGATCCCTCTCCACCCACTCTAGCAATCCCTTGGGGAGAGGCTGGGAGAA	114611
QY	3390	ATATAGATAGACACTGACATGAGCCCATTTGAGACACCTGGGGCCCACTGGACAAACNTG	3449
Db	11462	ATATAGATAGACACTGACATGAGCCCATTTGAGACACCTGGGGCCCACTGGACAAACNTG	115211
QY	3450	ATTCCTGGAGAGGTGGCTGGC--CCCAAGCTTCTCTCCCTGTGCACACACTGGACCCAC	3508
Db	11522	ATTCCTGGAGAGGTGGCTGGCCCCCAAGCTTCTCTCCCTGTGCACACACTGGACCCAC	115811
QY	3509	TGGCTGAGAAATCTGGGGGTGAGAGACAAAGAGAGAGAAATGTTCTCTGTGCCTG	3568
Db	11582	TGGCTGAGAAATCTGGGGGTGAGAGACAAAGAGAGAGAAATGTTCTCTGTGCCTG	116411
QY	3569	CTCCTGTACTTGTGCTCAGAGCTGGGGCTTCTCTCCCTCAATCAACCTTAACACTGACCT	3628
Db	11642	CTCCTGTACTTGTGCTCAGAGCTGGGGCTTCTCTCCCTCAATCAACCTTAACACTGACCT	117011
QY	3629	GGGGGTAGCCCCCGCCAGCCCTCAGTCA--CCCCACTTCCCACTTGCAGTCTGTAGCT	3687
Db	11702	GGGGGTAGCCCCCGCCAGCCCTCAGTCA--CCCCACTTCCCACTTGCAGTCTGTAGCT	117611
QY	3688	AGAACTTCTCTAAAGCTTAATACGTTTGTGTGAGATAAATATTTGGGATTTGGGGGAAAGAG	3747
Db	11762	AGAACTTCTCTAAAGCTTAATACGTTTGTGTGAGATAAATATTTGGGATTTGGGGGAAAGAG	118211
QY	3748	GAGCAAGGCCCCATAGACCTTGGGGGTGGGACATCTAGTACTGTGCACATTTGATTTT	3807
Db	11822	GAGCAAGGCCCCATAGACCTTGGGGGTGGGACATCTAGTACTGTGCACATTTGATTTT	118811
QY	3808	CTATAATCACTTGGGTTTGTACATTTTGGGGGAGAGACACAGATTTTATACACTATA	3867
Db	11882	CTATAATCACTT--GGGTTTGTACATTTTGGGGGAGAGACACAGATTTTATACACTATA	119401
QY	3868	TATGACACTAGCTTGAAGCAATTTTAATCCCTGTGACCTAGGCAAGTAAATATAAGGTTG	3927
Db	11941	TATGACACTAGCTTGAAGCAATTTTAATCCCTGTGACCTAGGCAAGTAAATATAAGGTTG	120001
QY	3928	AGTTTTCAC 3937	
Db	12001	AGTTTTCAC 12010	

GENERAL INFORMATION:
APPLICANT: Vogel, Wolfgang
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: LIGANDS FOR DISCOIDIN DOMAIN RECEPTOR TYROSINE KINASES
FILE REFERENCE: 11757.36USMO
CURRENT APPLICATION NUMBER: US/09/355,815
CURRENT FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: PCT/CA98/00093
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 60/041,578
PRIOR FILING DATE: 1997-02-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 3096
TYPE: DNA
ORGANISM: Homo sapiens
US-09-355-815-5

Query Match 16.2%; Score 642; DB 9; Length 3096;
Best Local Similarity 56.5%; Pred. No. 8.2e-173;
Matches 1534; Conservative 0; Mismatches 975; Indels 207; Gaps 10;

QY 349 TGGTCTGCTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGAGCATTTTGAATCTGCCA 408
DB 379 TGGTCTGCTCTCTGCTGCTGCTATCTTGATGTTCTGCAAAAGCTCAGATTAATCCACTA 438
QY 409 AGTGGCGGCTATGCTGCGGCGATGAGAGACCGGACATCCAGACAGTGAATCTGCTT 468
DB 439 TAGGCGGCTATGCTGCGGCGATGAGAGACCGGACATCCAGATTAATCCACTA 498
QY 469 CCAGCTCTGCTGATGATTCAGTCCGCGCCGACAGACAGTGGAGAGAGAGAGAGAGG 528
DB 499 CCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 558
QY 529 ATGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
DB 559 ATGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618
QY 586 TGGATATACAGACACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
DB 619 TGGATATACAGACACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
QY 646 GCGTGGGCAAGATCTCCCGGAGCTACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
DB 679 GTCATGCGCATCGATTTGCCCCATGATACAGATCAATTAATGAGTGGGATGCGCT 738
QY 706 GGAATGGGCTGAAGAGACCGCTGGGCTGAGAGTGAATCAAGCAATGAGAGACCGTGA 765
DB 739 GGAATGCTTGGGGAACCGTCAATGAGAAAGAGTGTGATGAGAAATGATTAACCCATG 798
QY 766 GAGTGGTGGTGAAGAGCTGGGCGCCCGCATGATGCTGCTGCTGCTGCTGCTGCTGCT 825
DB 799 AATTTTCTTAAGGAGCTGGAGCGCCCATGTTTACAGATTTGTCGCGTTCATTCAG 858
QY 826 GGGCTGACCGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
DB 859 TCACGAGACACATCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 918
QY 886 ATGAGCTCTGCTTACACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
DB 919 ATGGCTTGGTGTCTTACATGCTCCAGCTGGGAGAGTGTGATGATGATGATGATGATG 978
QY 940 CCGTATGCTCAACAGATTCAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATG 999
DB 979 TCATTTATCTGAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1037
QY 1000 GTCTGGCCAGCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059
DB 1038 --CTAGGCAATTAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1095
QY 1060 TGGGCGTCTGGCAGGCTATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1119

DB 1096 ACCAGTGTGGCCCGGCTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1155
QY 1120 ATGGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1179
DB 1156 ACATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1215
QY 1180 GTACACATGACACAGCTGGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1239
DB 1216 GCAACACATGATTTGTAAGAGTGAAGATCTTAAGAGATGATGATGATGATGATGATG 1275
QY 1240 GTGGCCGTGGCCGTGGAG 1299
DB 1276 CTG---AAGCAGTGAAGTGGAGACCTTAATGACATTTCTTCCCTGCTGCTGATGAG 1332
QY 1300 GGGACCCAG 1359
DB 1333 TCAACCCAG 1392
QY 1360 AGTCCGCTCTCTTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1419
DB 1393 AGTCTCAATGACATTTGACAGATGATGATGATGATGATGATGATGATGATGATGATG 1452
QY 1420 ATGTGGAACAATTCCTCCGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1479
DB 1453 ATGCTGCAATGATACACACTGTAAGCCCTGCGCCACTCTTC----- 1495
QY 1480 CGCTGGCCACCTCCACCAACTTCAGAGCTTGGAGCTGGAGAGAGAGAGAGAGAGAG 1539
DB 1496 -----TAGGACCCACAACTATGATC 1518
QY 1540 CCGTGGCCAG 1599
DB 1519 CAGTCTTAAGTGAAG 1578
QY 1600 TCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1659
DB 1579 TCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1638
QY 1660 TCAGAGAGCTGAAG 1719
DB 1639 TGGAGAGAGCTTCGAGAGAGATGCTGATGATGATGATGATGATGATGATGATGATG 1698
QY 1720 GGGACATTCATGATCAACACCGCCAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAG 1779
DB 1699 GTGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1731
QY 1780 CCGGCGCTGCTGAG 1839
DB 1732 CAGTCACTGATGAG 1778
QY 1840 TGGTCTCAATCCAGCTTACCGCTCTTGGCCACTTACGCGCGTCCCGCTGAGAGAG 1899
DB 1779 -----CCCTTCGCGC 1788
QY 1900 CGGCGCCCGCCACACCGCGCTGGGCAACCAACCAACCAACCAACCAACCAACCAACCA 1959
DB 1789 CTGACTACCAAG 1848
QY 1960 ATATGAGAGCTGAAG 2019
DB 1849 AG 1908
QY 2020 CCGATTAATGAG 2079
DB 1909 CCGATTAATGAG 1968
QY 2080 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2136
DB 1969 CAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2028
QY 2137 CTGAGATGAG 2196

QY 2916 TTTCTCCGAGACGAGGCGGAGGATGATCTGTCCCGCCGCTGCTGCCGAGAGG 2975
 DB 2891 TTTCTCCGAGACGAGGCGGAGGATGATCTGTCCCGCCGCTGCTGCCGAGAG 2950
 QY 2976 CATTATGAGCTATCTCTGCTGCTGAGAGCCGAGAGTCTGAGCAGCAGCCTTTCC 3035
 DB 2951 GTGTATGAGCTATCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3010
 QY 3036 CAGTCATCGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3084
 DB 3011 GAAATACACCT 3059

RESULT 9
 US-09-815-343-505/c
 ; Sequence 505, Application US/09815343
 ; Patent No. US20010055596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meagher, Madeline
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: King, Gordon E.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE REFERENCE: 21021.304
 ; CURRENT APPLICATION NUMBER: US/09/815.343
 ; PRIORITY FILING DATE: 2001-03-22
 ; NUMBER OF SEQ ID NOS: 1556
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 505
 ; LENGTH: 563
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(563)
 ; OTHER INFORMATION: n - A,T,C or G
 US-09-815-343-505

Query Match 13.2%; Score 522.8; DB 10; Length 563;
 Best Local Similarity 97.7%; Pred. No. 4.8e-139;
 Matches 549; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 511 TGGAGAGCAGTGCAGGAGATGGGCGC-TGGTCCCGCAGAGGTCGTTTCCC-AAAGA 568
 DB 562 TGAANAACAGTACGAGGATGGGCGCTGTGTCGCCGAGAGGTCGTTTCCCAGAGA 503
 QY 569 GAGAGAGTACTTGCAGGTGATCTTCAACAGCAGTGCAGTGTGTTGGTGGCAGCCA 628
 DB 502 GAGAGAGTACTTGCAGGTGATCTTCAACAGCAGTGCAGTGTGTTGGTGGCAGCCA 443
 QY 629 GAGAGAGTACTTGCAGGTGATCTTCAACAGCAGTGCAGTGTGTTGGTGGCAGCCA 688
 DB 442 GAGAGAGTACTTGCAGGTGATCTTCAACAGCAGTGCAGTGTGTTGGTGGCAGCCA 383
 QY 689 CCGGAGTGTGCGCGCTGATGGCTGGAAGAGCCGCTGGGCTAGAGAGTGTACTCAGG 748
 DB 382 CCGGAGTGTGCGCGCTGATGGCTGGAAGAGCCGCTGGGCTAGAGAGTGTACTCAGG 323
 QY 749 CAATGAGAGACCTGAGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 808
 DB 322 CAATGAGAGACCTGAGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 263
 QY 809 GGTTCGCTTACACCGCCGCTGATGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 868
 DB 262 GGTTCGCTTACACCGCCGCTGATGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 203
 QY 869 TGGCTGCTTACACCGCCGCTGATGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 928
 DB 202 TGGCTGCTTACACCGCCGCTGATGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 143
 QY 929 TTTATGAGAGCCGCTGATGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 988
 DB 142 TTTATGAGAGCCGCTGATGAGAGTGTGCTTACACCGCCCTTGGGGCAGACATGTA 83

QY 989 GCAGTATGGGGCTTGGGCGACCTGCGACATGTGTGTGGGCTGATGACTTTAGCA 1048
 DB 82 GCAGTATGGGGCTTGGGCGACCTGCGACATGTGTGTGGGCTGATGACTTTAGCA 23
 QY 1049 GAGTCAGAGCTGCGGGTCTGG 1070
 DB 22 GAGTCAGAGCTGCGGGTCTGG 1

RESULT 10
 US-09-771-161A-14
 ; Sequence 14, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771.161A
 ; PRIORITY FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 2083
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-771-161A-14

Query Match 9.1%; Score 361.4; DB 10; Length 2083;
 Best Local Similarity 57.0%; Pred. No. 9.7e-93;
 Matches 802; Conservative 0; Mismatches 536; Indels 69; Gaps 5;

QY 349 TGTCTCTCTCTCTGTCGTCGATGATGATGATGATGATGATGATGATGATGATGAT 408
 DB 379 TGTCTCTCTCTCTGTCGTCGATGATGATGATGATGATGATGATGATGATGATGAT 438
 QY 409 AGTCCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
 DB 439 TATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
 QY 469 CGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
 DB 499 CGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 558
 QY 529 ATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
 DB 559 ATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618
 QY 586 TGTATCTCAACAGCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
 DB 619 TGTATCTCAACAGCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
 QY 646 GCTTGGGAGAGAGTCTTCCCGAGCTACCGGCTGCTTACTCCCGGATGGTGGCGCT 705
 DB 679 GCTATGGAGATGAGATTTCCCGAGCTACCGGCTGCTTACTCCCGGATGGTGGCGCT 738
 QY 706 GATGAGGCTGGAAGAGCCGCTGAGAGTGTGATGATGATGATGATGATGATGATGAT 765
 DB 739 GATGAGGCTGGAAGAGCCGCTGAGAGTGTGATGATGATGATGATGATGATGATGAT 798
 QY 766 GATGAGGCTGGAAGAGCCGCTGAGAGTGTGATGATGATGATGATGATGATGATGAT 825
 DB 799 ACATTTTCTTAAAGAGCTTGAAGCCCGCATTTGATGATGATGATGATGATGATGAT 858
 QY 826 GGGCTGACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 885
 DB 859 TCACGACAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 918

Query Match 5.9%; Score 232.8; DB 10; Length 387;
 Best Local Similarity 82.5%; Pred. No. 2.8e-56;
 Matches 315; Conservative 0; Mismatches 62; Indels 5; Gaps 4;

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OY 3453 CCTGAGAGGGGGGCGC--GGCCGAGCTTCTCTCCCTGTCACACTGGAGCCOACTG 3510
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Db 386 CCTGAGAGAGAGGCTGCGCCGCCAGCCCTCTCTCCGTCACACTGGAGCCOACTG 327
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OY 3511 GCTGAGATCTGGG-GGTGAGAGAGACAAGAGAGAGAAATGTTCTGTCCTGC 3569
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Db 326 GCTGAGATTTGGGAGAGAGAGACAAAGAGAGAGAGGGGTTCCCTGTATCTCC 267
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OY 3570 TCCTGTACTTGTCTCAGCTTGGGCTTCTCTCCATGACCTGAACAACCTG 3629
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Db 266 TCCTGSAATTCCTCAGCTTGGGCTTCCCTCTCTCATCTCTGAACAACCTG 207
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OY 3630 GGGGT-AGCCCCGCCCCAGCCCTCAGTACCCCACTTCCCACTTGCACTTGTAGCTA 3688
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Db 206 GGGGTGATCCCTACCCCACTTCTGCTCCCACTCCCACTGCGGTGTAGCTA 147
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OY 3689 GAATTCCTAAGCTTACGTTCTGTGAGTAATAATTTGGATT-GGGGGAAAGAG 3747
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Db 146 GAATTCCTCAAGCTTATATTTCTGTGAATTAATTTGGATTAGCGGGAAACAGA 87
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OY 3748 GAGCAAGGGCCATAGCTTGGGTTGGACATCTAGTGTAGTCCACATTGATTTT 3807
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Db 86 GAGCAAGGGCCCTGTGGCCCTGGGTTGGACATCTAGTGTAGTCCACATTGATTTT 27
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OY 3808 CTATATCATCTTGGGTTTGA 3829
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Db 26 CTATATCATCTTGGGTTTGA 5
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Search completed: May 30, 2003, 16:10:26
 Job time : 506 secs